

SEQUENCE LISTING

<110> Ptacek, Louis J.
Fu, Ying-Hui
Jones, Christopher R.

<120> Casein Kinase I Delta and Casein Kinase I Epsilon and Sleep in Humans

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 <213> Homo sapiens

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 cgggcggctc cgcgaatcct ccggcatccg ccccggcggg ccgccccgc ccgcggcagc 180
 ccccgagca gtggcccggc atcggcgctt tcccggcggg caagagtgg ccatggagct 240
 acgtgtgggg aacaagtacc gcctgggacg gaagatcggg agcgggtcct tcggagatat 300
 ctacctgggt gccaacatcg cctctggtga ggaagtcgcc atcaagctgg agtgtgtgaa 360
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 ggggatcccg tccatcaagt ggtgcggagc tgagggcgac tacaacgtga tggatcatgga 480
 gctgctgggg cctagcctcg aggacctgtt caacttctgt tcccgcaa atcagcctcaa 540
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 cttcatccac cgggacgtca agcccgacaa cttcctcatg gggctgggga agaagggcaa 660
 cctggtctac atcatcgact tcggcctggc caagaagtac cgggacgccc gcaccacca 720
 gcacattccc taccgggaaa acaagaacct gaccggcacg gcccgctacg cttccatcaa 780

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 agcctcacag acaagtgtgc catttgacca tctcggaag tgaggagagc cccattgga 1500
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<210> 10
 <211> 416
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Glu Leu Arg Val Gly Asn Lys Tyr Arg Leu Gly Arg Lys Ile Gly
 1 5 10 15

Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Ala Asn Ile Ala Ser Gly
 20 25 30

Glu Glu Val Ala Ile Lys Leu Glu Cys Val Lys Thr Lys His Pro Gln
 35 40 45

Leu His Ile Glu Ser Lys Phe Tyr Lys Met Met Gln Gly Gly Val Gly
 50 55 60

Ile Pro Ser Ile Lys Trp Cys Gly Ala Glu Gly Asp Tyr Asn Val Met
 65 70 75 80

Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
 85 90 95

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
 100 105 110

Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
 115 120 125

Val Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
 130 135 140

Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
 145 150 155 160

Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
 165 170 175

Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
 180 185 190

Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
 195 200 205

Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
 210 215 220

Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
 225 230 235 240

Cys Lys Gly Tyr Pro Ser Glu Phe Ser Thr Tyr Leu Asn Phe Cys Arg
 245 250 255

Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ser Tyr Leu Arg Gln Leu
 260 265 270

Phe Arg Asn Leu Phe His Arg Gln Gly Phe Ser Tyr Asp Tyr Val Phe
 275 280 285

Asp Trp Asn Met Leu Lys Phe Gly Ala Ala Arg Asn Pro Glu Asp Val
 290 295 300

Asp Arg Glu Arg Arg Glu His Glu Arg Glu Glu Arg Met Gly Gln Leu
 305 310 315 320

Arg Gly Ser Ala Thr Arg Ala Leu Pro Pro Gly Pro Pro Thr Gly Ala
 325 330 335

Thr Ala Asn Arg Leu Arg Ser Ala Ala Glu Pro Val Ala Ser Thr Pro
 340 345 350

Ala Ser Arg Ile Gln Pro Ala Gly Asn Thr Ser Pro Arg Ala Ile Ser
 355 360 365

Arg Val Asp Arg Glu Arg Lys Val Ser Met Arg Leu His Arg Gly Ala
 370 375 380

Pro Ala Asn Val Ser Ser Ser Asp Leu Thr Gly Arg Gln Glu Val Ser
 385 390 395 400

Arg Ile Pro Ala Ser Gln Thr Ser Val Pro Phe Asp His Leu Gly Lys
 405 410 415

<210> 11
 <211> 1559
 <212> DNA
 <213> Homo sapiens

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 cgggcggctc cgcgaatcct ccggcatccg ccccggcggg ccgccccgc ccgcggcagc 180
 cccccgagca gtggccccgc atcggcgcct tcccggcggg caagagtgg ccatggagct 240
 acgtgtgggg aacaagtacc gcctgggacg gaagatcggg agcgggtcct tcggagatat 300
 ctacctgggt gccaacatca cctctggtga ggaagtcgcc atcaagctgg agtgtgtgaa 360
 gacaaagcac cccagctgc acatcgagag caagttctac aagatgatgc aggggtggcgt 420
 ggggatcccg tccatcaagt ggtgcggagc tgagggcgac tacaacgtga tggatcatgga 480
 gctgctgggg cctagcctcg aggacctgtt caacttctgt tccgcaaat tcagcctcaa 540
 gacggtgctg ctcttgggcg accagatgat cagccgcac gagtatatcc actccaagaa 600
 cttcatccac cgggacgtca agcccgacaa cttcctcatg gggctgggga agaagggcaa 660
 cctggtctac atcatcgact tcggcctggc caagaagtac cgggacgccc gcaccaccca 720
 gcacattccc taccgggaaa acaagaacct gaccggcacg gcccgctacg cttccatcaa 780

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cacgcacctg ggcattgagc aaagccgtcg agatgacctg gagagcctgg gctacgtgct      840
catgtacttc aacctgggct ccctgccctg gcaggggctc aaagcagcca ccaagcgcca      900
gaagtatgaa cggatcagcg agaagaagat gtcaacgccc atcgagggtcc tctgcaaagg      960
ctatccctcc gaattctcaa catacctcaa cttctgccgc tccctgcggt ttgacgacaa     1020
gcccgactac tcttacctac gtcagctctt ccgcaacctc ttccaccggc aggggttctc     1080
ctatgactac gtctttgact ggaacatgct gaaattcggg gcagcccgga atcccagagga     1140
tgtggaccgg gagcggcgag aacacgaacg cgaggagagg atggggcagc tacggggggtc     1200
cgcgacccga gccctgcccc ctggcccacc cacggggggcc actgccaacc ggctccgcag     1260
tgccgccgag cccgtggctt ccacgccagc ctcccgcatc cagccggctg gcaatacttc     1320
tcccagagcg atctcgcggg tcgaccggga gaggaagggt agtatgaggc tgcacagggg     1380
tgcgcccgcc aacgtctcct cctcagacct cactgggcgg caagaggtct cccggatccc     1440
agcctcacag acaagtgtgc catttgacca tctcggaag tgaggagagc cccatttga      1500
ccagtgtttg cttagtgtct tcaactgtatt ttctttaaaa aaaaaaaaaa aaaaaaaaaa     1559

```

```

<210> 12
<211> 416
<212> PRT
<213> Homo sapiens

```

```
<400> 12
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```

Met Glu Leu Arg Val Gly Asn Lys Tyr Arg Leu Gly Arg Lys Ile Gly
1           5           10           15

```

```

Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Ala Asn Ile Thr Ser Gly
          20           25           30

```

```

Glu Glu Val Ala Ile Lys Leu Glu Cys Val Lys Thr Lys His Pro Gln
35           40           45

```

```

Leu His Ile Glu Ser Lys Phe Tyr Lys Met Met Gln Gly Gly Val Gly
50           55           60

```

```

Ile Pro Ser Ile Lys Trp Cys Gly Ala Glu Gly Asp Tyr Asn Val Met
65           70           75           80

```

```

Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
          85           90           95

```

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
100 105 110

Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
115 120 125

Val Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
130 135 140

Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
145 150 155 160

Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
165 170 175

Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
180 185 190

Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
195 200 205

Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
210 215 220

Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
225 230 235 240

Cys Lys Gly Tyr Pro Ser Glu Phe Ser Thr Tyr Leu Asn Phe Cys Arg
245 250 255

Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ser Tyr Leu Arg Gln Leu
260 265 270

Phe Arg Asn Leu Phe His Arg Gln Gly Phe Ser Tyr Asp Tyr Val Phe
275 280 285

Asp Trp Asn Met Leu Lys Phe Gly Ala Ala Arg Asn Pro Glu Asp Val
290 295 300

Asp Arg Glu Arg Arg Glu His Glu Arg Glu Glu Arg Met Gly Gln Leu
305 310 315 320

Arg Gly Ser Ala Thr Arg Ala Leu Pro Pro Gly Pro Pro Thr Gly Ala
325 330 335

Thr Ala Asn Arg Leu Arg Ser Ala Ala Glu Pro Val Ala Ser Thr Pro
340 345 350

Ala Ser Arg Ile Gln Pro Ala Gly Asn Thr Ser Pro Arg Ala Ile Ser
355 360 365

Arg Val Asp Arg Glu Arg Lys Val Ser Met Arg Leu His Arg Gly Ala
370 375 380

Pro Ala Asn Val Ser Ser Ser Asp Leu Thr Gly Arg Gln Glu Val Ser
385 390 395 400

Arg Ile Pro Ala Ser Gln Thr Ser Val Pro Phe Asp His Leu Gly Lys
405 410 415